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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: April 1, 2003, 08:49:06 ; search time 93.5 Seconds (without alignments)

6121.913 Million cell updates/sec

Title: US-09-768-781-2 .

Perfect score: 2543

Sequence: 1 atgaaacacaaagaccacaaaca.....caaggccaaagtgttgtctga 1389

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Eqapop 6.0 , Eqapext 7.0

Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 20604715 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Command line parameters:

```

-MODEL=frame+ n2p model
-DB=US09768781/app_query.fasta_1.1543
-Q=0/gnn2.1/USP0/app_query.fasta_1.1543
-DB=SPTRMBL2 -QFMM=fasian -SUFFP=cln=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blobsum62 -TRANS=human40_cdi
-LIST=45 -DOCALL=200 -TRN_SCORE=pct -THR_MAX=1.00 -THR_MIN=0 -ALIGN=15
-MODB=LOCAL -OUTFMT=pro -NORM=ext
-USEB=US09768781@CGEN 1.1.158 @runt 01042003 084730 4939 -NCPU=6 -ICPU=3
-NO_XLPPX -NO_MM -LARGEBS=1 -NEG_SCORES=0 -WAIT -LONGLOG -DEV -TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

Database : SPTRMBL21:\*

- 1: sp\_archea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rrodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

09h6d3 homo sapien

096p28 homo sapien

017386 caenorhabdi

08r118 mus musculus

09sak8 arabidopsis

09vic2 pyrococcus

048339 oryza sativa

0942c7 oryza sativa

09b828 schistosoma

09n95 schistosoma

094ux1 schistosoma

094ux2 schistosoma

094ux6 schistosoma

094ux7 schistosoma

094ux8 schistosoma

047543 chlamydomon

0980c2 mycoplasma

02106 pygathrix b

09b509 terodontop

006039 lactococcus

098837 arabidopsis

021815 pygathrix b

021707 pygathrix b

0955c7 cheirogaleu

08r12 arabidopsis

021708 pygathrix b

09q111 cercopithecus

QBxM39 clostridium

QBxM39 salmonella

0955f8 cheirogaleu

Q9f821 clostridium

Q19463 caenorhabdi

0994e7 porcine ade

Q9pw3 neurospora

Q87v5 escherichia

Q99xh1 streptococcus

Q82874 salmonella

Q96317 schistosoma

Q955f9 cheirogaleu

Q9x0k3 bacteroides

Q8sey6 bombyx mand

#### ALIGNMENTS

RESULT 1  
Q9QXY7  
ID Q9QXY7  
PRELIMINARY, PRT; 446 AA.  
AC Q9QXY7;  
DT 01-MAY-2000 (TRIMBLrel. 13, Created)  
DT 01-MAY-2000 (TRIMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TRIMBLrel. 17, Last annotation update)  
DE Q9QXY7  
GN XK antigen (1810038K19RIK protein).  
OS Mus musculus (Mouse).  
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Butherida; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10096;

[1] SEQUENCE FROM N\_A

[2] SEQUENCE FROM N\_A

RC STRAIN=BALB/C; TISSUE=SKELETAL MUSCLE;

RX MEDLINE=200009522; PubMed=0541802;

RA Collec E., Colin Y., Carbonnel F., Hattab C., Bertrand O.,

RA Cartron J.P., Kim C.-I.;

RT "Structure and expression of the mouse homologue of the XK gene." ;  
RT Immunogenetics 50:16-21 (1999).

RN [1]

RN [2]

RC STRAIN=BALB/C; TISSUE=SKELETAL MUSCLE;

RA Le Van Kim C., Collec E., Colin Y.;

RA

#### SUMMARIES

Result No.	Query Match Length	DB ID	Description
1	953.5	37.5 446 11	Q9QXY7 mus musculus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### RESULTS



RC TISSUE=SKIN;  
 RA straenber R.;  
 RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 [3]  
 SEQUENCE FROM N.A.  
 TISSUE=SKIN;  
 straenber R.;  
 Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AK028024; BAH15326.; -;  
 DR EMBL; BC013379; AAH13379.1; -;  
 DR EMBL; BC028564; AAH28564.1; -;  
 DR Heterological protein;  
 DR 395 AA; 44654 MW; 23199BAEEA6964C6 CRC64;  
 SQ SEQUENCE

Alignment Scores:	
Pred. No.:	Length:
Score:	1.87e-06
Percent Similarity:	158.50
Best Local Similarity:	38.33%
Query Match:	20.26%
DB:	6.23%
DB:	4
DB:	4
DB:	21

Qy US-09-768-781-2 (1-1389) x Q9HCD3 (1-395)

Qy 91 TCTCTGGAGAAAGATGTCATCCGTGGGCCAACCCGATTTACTTTCCAT  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 8 AlleleLeuArgAspLeuValLeuGly-----  
 Qy 151 CTTCTCCACTTTGTACTGTGGGAGGCTGATCTGTTGACATGG  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 17 ValLeuGlyThrAlaAlaPheLeuAspLeuGlyThrAspLeuTrpAlaA  
 Qy 211 TATCGAAAGATAATGTGAAACTACTGGATGACATACACCTTTCTCTCTTA  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 37 TyrAlaLeuGlyArgTyrLeuTrpAlaAlaLeuValLeuAlaLeuLeuG  
 Qy 271 TCATTATGTCAGTTG---ACCCATTTGTGCAAGAGAT-----  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 57 SerValAlaLeuGlnLeuPheSerTrpLeuArgAlaAspProAlaG  
 Qy 319 AAAGATAAACCG-----CTATCATTATTTATGCTATTAATCTCTCT  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 77 GlySerGlnProArgArgGlySerLeuAlaLeu---LeuIleLeuGlnL  
 Qy 367 GTATCAGATGTTGAGGCCATGTTAAAGTACCTCAGACTGTTGAGAAAGG  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 96 LeuTyrArgCysValGlnGluLeuArgGlnGlyLeuLeuValLeuP  
 Qy 427 GAGAGCCCTATGTGCCCACCCGAAAGAAGATGCTAAATAGATGGCGGG  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 113 GluGluPro-----  
 Qy 487 ATAGAAATGGAGGAGGGGCAACTCCATCGGCCAACCTTGGCTATGCCGACATGG  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 116 SergIupheAspLeuAlaAlaTyrAla---AspPheLeuAlaLeuAsp-----  
 Qy 547 CGATGTCAGATCAGTCAGTCAGCTCCGGTCACTGGCTCTGGGTAGTCCCAGCTGACCTATC  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 132 MetLeuArgLeuPheGluLysPheLeuGluLysAlaProClnLeuThrLeuV  
 Qy 607 GTAGCCCTGATCTCTGCAAGGGTCCCTGGGTAGTGGCTTAATGGTAT  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 152 IleMetLeuGlnSerGlyArgAlaLglutryrGlyLeuTrpGlyIleCyst  
 Qy 667 GTCATGTCACCCATTGGGCCACCCCTTGCATATGTTGGCTATTCAGATCA  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 172 LeuGlyIleSerTrpAlaLeuLeu-----  
 Qy 727 GACTAC-----AAGATTGCGCTTGGGC  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 180 AspTyrIleArgIleLeuArgIleCysLeuProSerLeuProLeuLeuIleL  
 Qy 757 GTCCCTCTGTCATCACCATCGGGCACATGGGACTACTCCGACTTCACT  
 ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Alignment Scores:	Length:
Pred. No.:	8.48e-05
Score:	141.50
Percent Similarity:	42.41%
Length:	505
Matches:	65
Conservative:	69

Alignment Scores:  
Pred. No.:  
Score:  
Percent Similarity:



### Alignment Scores:

Pred. No.:	0.000128	Length:	362
Score:	129.0	Matches:	58
Percent Similarity:	40.98%	Conservative:	42
Best Local Similarity:	23.77%	Mismatches:	100
Query Match:	5.07%	Indels:	44
DB:	11	Gaps:	9
US-09-768-781-2 (1-1389) x Q8R118 (1-362)			
Qy 559 ATCCAGGCCCTCCTGGCTCACTGCCCCAGCTGACCTATGAGCTCTATGAGCCGTGATC 618			
Db 14 LeuGluThrLeuGluSerAlaProinLeuValLeuGlnLeuCysMetFilegln 33			
Qy 619 TCTGCAGAGGTCCCTGGTGAAGTGTGCTTAATGGTATTTCCCTGCTGATCTGTCAAC 678			
Db 34 LysAsnSerAlaGluThrLeuProCysValSerSerThrSerLeuMetSerLeuAla 53			
Qy 679 TATGGGGCCACCCCTTGCATATTGCTGCTCACTAGTACAAGATT 738			
Db 54 TrpValLeuAlaSerTyhiSoyLeu--LeuArgAspSerArgAspSlys-- 71			
Qy 739 CGCCCTGGCCCACTAGAAGTCTCTGCATACCATTGGGACATGGAGATCACTTC 798			
Db 72 SerMetSerTyArgGlyAlaLeuLeuHisLeuPheTrpArgLeuPheThrIleSerSer 91			
Qy 799 CGCTCTGATTCTGGCTCTCTGACCACTTTGAAATTGAGGCTGTGCCCTTCCTA 858			
Db 92 ArgValLeuSerPheAlaLeuPheAlaSerIleLeuPheGlnLeuTyPheGlyIlePheVal 111			
Qy 859 GTGCTCAACTCCCTGATCATCTCTTGGCCCTGGAATTAGTTCTGAGAAGTGGGCC 918			
Db 112 ValValHisTrpCysAlaMetAlaPhe----TrpIleIleHisGlyGlyThrAspPhe 129			
Qy 919 CAGATGCCAATAAACATTGAGAAAAACTCTGGGGACTCTGCTGCTGAT 978			
Db 130 CysMetSerLysTrpGluGlyIleLeuPheAlaSerMetVal----- 142			
Qy 979 TCACTCACCATCCTCTGTCATCAACTCTCTCTGCTGCTCAGGTGAGG 1038			
Db 143 ---ValGlyIleValIyr-----11LePheCysTrpPheAsn----- 153			
Qy 1039 TTGGCAGACAGAGATCTGTCACAAGGGCAGAACCTGGGACATATGGCTGCACTA 1098			
Db 154 -----ValLeuGluGlyArgThrArgTyPheAlaTyTy 167			
Qy 1099 AGTGTGAGTTGGTAGAGAATCTGATCATGGCTCTGGTTTAAGTTC----- 1146			
Db 168 ThrIleValLeuThrGluAlaAlaLeuThrPheLeuTrpPheTyArgAsnPro 187			
Qy 1147 -----TTTGGAGTTGAAAGTGTACTGATTAATGCTATGCTTCTGATGTC 1191			
Db 188 GluSerThrAspSerTyAlaValProAlaLeuCys-----Cys----- 200			
Qy 1192 TTGCAAGCTCATATTATGGCTATGATTTCATGCTCTTCCAGTAC 1251			
Db 201 -----ValPheValSerPheValAlaGlyIleIleLeuMetLeuIeuryrGlyVal 218			
Qy 1252 TTGCATCCATG 1263			
Db 219 LeuHisProMet 222			
RESULT 7			
Q9SAK8 ID Q9SAK8 PRELIMINARY;			
Q9SAK8 AC			
DT 01-NAY-2000 (TREMBLref. 13, Created)			
DT 01-NAY-2000 (TREMBLref. 13, Last sequence update)			
DT 01-DEC-2001 (TREMBLref. 19, Last annotation update)			
DE T8K14-18 protein.			
GN T8K14-18			
OS Arabidopsis thaliana (Mouse-ear cress);			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC			
179 GlyArgLeuThrIleSerCysAlaLeuPheIleGluLeuThrAsnValValLeuThr 198			
805 CTGATTCCTGCTGCTCTCTGAGCCCTTCTGAGCTTCTGCTCTAGTGTGCTC 864			
199 IleIleMetAlaPheIleSerGlyIleLeuPheLeuLeuLeuAla 218			
694 TGCATAATGTTGGCTATCCAGTACAGTACAGTACTACAGATT-----CGCCTT 744			
Db 165 ValArgSerIleAla-----AspProTrpIleSerLeuSerThrCysGluIle 178			
745 GGGCACTGAACTGCTCTGCTACATCAGTCTGGGACACATGGAGATCACTCCGCCTC 804			
Db 179 GlyArgLeuThrIleSerCysAlaLeuPheIleGluLeuThrAsnValValLeuThr 198			
805 CTGATTCCTGCTGCTCTCTGAGCCCTTCTGAGCTTCTGCTCTAGTGTGCTC 864			
199 IleIleMetAlaPheIleSerGlyIleLeuPheLeuLeuAla 218			
865 AACCTCCGATCATCCTCTTGAGTAACTGGGATTAAGTTCTGGAGAGT 918			



Db	330	AsnAlaValGlnAsnValSerThrPheLeuGlyLeuPhePheGlyLeuAlaTyrSer	349
Qy	1165	CTGATTACTGTCATCCCTGATTGCTTGCAGCTTATTATTGCTTATCTGATTCCATT	1224
Db	350	LeuGlyGlueLeuLysSerLileIleThrValAsnLeuGlyLeuAlaSerPheLeuProhe	369
Qy	1225	GGCTTCATGGCTCCCT	1239
Db	370	SerIleAlaLeuIle	374
RESULT	9		
	048539	PRELIMINARY;	PRT; 745 AA.
	AC	048539;	
	DT	01-JUN-1998 (T-EMBLrel. 06, Created)	
	DT	01-JUN-1998 (T-EMBLrel. 06, Last sequence update)	
	DT	01-MAR-2002 (T-EMBLrel. 20, Last annotation update)	
	DE	RbohD5P (Fragment).	
	OS	Oryza sativa (Rice)	
	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
	OC	Ehrhartoideae; Oryzae; Oryza.	
	OX	NCBI_TaxID=4530;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RA	Keller T, Damude H G, Werner D, Doerner P, Dixon R A, Lamb C.;	
	RT	"A plant homolog of the neutrophil NADPH oxidase with gp91phox subunit genes encodes an intrinsic plasma membrane protein with Ca2+-binding and RangA1 domains."	
	RT	Submitted (JUL-1997) to the ENBL/GenBank/DBJ databases.	
	RL	EMBL: AF015302; AAB7790.1; -.	
	DR	InterPro; IPR002048; BP-hand.	
	DR	InterPro; IPR002916; Ferric_reduct.	
	DR	InterPro; IPR000778; Gp91phox.	
	DR	Pfam; PF00036; ehand; 1	
	DR	Pfam; PF01794; Ferric_reduct; 1.	
	DR	PRINTS; PRO0466; GP91PHOX.	
	DR	PROSITE; PS00018; EP_HAND; UNKNOWN_1.	
	FT	NON_TER 1	
	SEQUENCE	745 AA; 85335 MW; 8734D3E13A46B3B2 CRC64;	
		Alignment Scores:	
		Pred. No.:	0.00954
		Score:	120.50
		Percent Similarity:	36.44%
		Best Local Similarity:	20.74%
		Query Match:	4.74%
		DB:	10
		SEQUENCE	15
		Length:	745
		Matches:	78
		Conservative:	59
		Mismatches:	144
		Indels:	95
		Gaps:	15
	US-09-768-781-2 (1-1389) x 048539 (1-745)		
Qy	310	GATCTAGCCAAAGATAAACCCCTATCATTATTGCTCATCTAAATCTCTGGACCTGTT	369
Db	58	ABPnserPheAspSerArgLeuGlnIlePhePheGluMetValAspLysAsnAlaAsp	77
Qy	370	ATCAGATGTTGGAGGCCATGATTAAAGTACCTC-----	
Db	78	GlyArgIleThrGluAlaGluValysGluIleMetLeuSerAlaAsnLys	97
Qy	406	CTGTGAGAAAGAGGAGCTGGAGCTGGAGCTGGCCACTCCATCCGGACCTGGCT	465
Db	98	LeuSerArgLeuIleGluGlnAlaGluIutyrAlaAlaLeuIleMetGluGluLeuAsp	117
Qy	466	ATAGATGGCCGGAGCTGGCTGATGAGATGGAGGTGGCCACTCCATCCGGACCTGGCT	525
Db	118	ProGlyLeuGlyIutyrIleGluLeuIleLeuIleLeuIleLeuIleLeuIleLeuIle	133
Qy	526	ATGGCACCCGCAATGCCATCAAACGTATGTCAGATC-----	-CAAGCCTRC 570
Db	134	LeuGlnIlyBspThrIutyrMetAsnTyrSerGlnAlaLeuSerTyrThrSerGlnIleIle	153
Qy	571	CTGGCCCTAGGCCCAAGCTGACCTGATGTCAGAGTT	630

"*Oryza sativa* nipponbare (GA3) genomic DNA, chromosome 1, BAC clone: B10G0H01." Submitted (May-2001) to the EMBL/GenBank/DBJ databases.

QY	892	TGGATTAAGCTTCTGGAAACTGGTCCCAAGATGCCAAATACATTGAAAACATTCAGC 951
Db	444	Triplearginserthargalaalaargalaaleuprophenaspasparnileasnphenis 463
QY	952	CGGTCTGGCACTCTGGCTGATTCAGTCACCATCCTCTATGCGCATCAACTC 1011
Db	464	LysthrileAlaAlaAlaAlaValValGlyle--IleLeuHisAlaGlyAsnHisIleu 482
QY	1012	TCTTGTGTCAGCTTGCAGTCAGTGGAGAGATCTCGACAAAGGGAG 1071
Db	483	ValcysAspPheProArgLeuIleysSerAspPheGluIleystyralaProIleGlyIle 502
QY	1072	AACTGGGACATATGGCTGCACTAT-----AGTGAGGTGGTAGAG 1116
Db	503	TyrPheGlyGluIleysPheThrLeuIvalysGlyValGluGlyIleThr 522
QY	1117	AATGTGATCATGGCTCTGGTTTT-----1140
Db	523	GlyAlaIleMetValIcysMetIleIleAlaPheIleAlaPheThrArgTrpPheArg 542
QY	1141	-----ANGTTCTTGGAGTGAAGTGTACTG 1167
Db	543	ArgSerIleVallysLeuProArgProPheAspIleLeuThrGlyPheAsnAlaPheIrp 562
QY	1168	AATTACTGTCTATTCCTTG-----1206
Db	563	--TyrSerHisIleLeuPheIleValThrIleAlaLeuIleValHisGlyGluCys 581
QY	1207	GCTTATCTGATTTCATGGCTTCATGCCCTCTTCAGCTCTCCAGTACTG 1254
Db	582	LeytyrLeuIleHisValTrpTyraGArgThrPheGlyIleThrPheTrpIleLeu 597
RESULT 11		
Q9B8Z8		PRELIMINARY; PRT; 424 AA.
AC	Q9B8Z8	
DT	01-JUN-2001	(TREMBL) 1. 17, Created)
DT	01-MAR-2002	(TREMBL) 1. 20, Last annotation update)
DE	NADH-ubiquinone oxidoreductase	chain 4 (EC 1.6.5.3).
GN	NAD4	
OS	Schistosoma japonicum	(Blood fluke).
OG	Mitochondrion.	
OC	Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidaida;	
OC	Schistosomatidae; Schistosomatidae; Schistosoma.	
NCBI_TaxID	61822;	
RN		
RP	SEQUENCE FROM N.A.	
RC	STRAIN=ANHII;	
RX	PubMed=10889225;	
RA	Le T.H., Blair D., Agatsuma T., Humair P.F., Campbell N.J.,	
RA	Iwagami M., Littlewood D.T., Peacock B., Johnston D.A., Bartley J.,	
RA	Rollinson D., Herniou E.A., Zarlinga D.S., McManus D.P.,	
RT	"Phylogenies inferred from mitochondrial genes orders-a cautionary tale from the parasitic flatworms."	
RT	from the parasitic flatworms."	
RL	InterPro; IPR003918; AAC13139.2	
DR	NADH oxidored4.	
DR	InterPro; IPR001750; NADH oxidored4.	
DR	PFam; PF0361; oxidored4.	
DR	PRO1337; NDOQGDRATSE4.	
KW	Mitochondrion; NAD; Oxidoreductase; Ubiquinone.	
SEQUENCE	424 AA;	3777C53E61F57D72 CRC64;
Alignment Scores:		
Pred. No.:	0.0108	Length: 424
Score:	119.50	Matches: 91
Percent Similarity:	36.36%	Conservative: 77
Best Local Similarity:	19.70%	Mismatches: 155
Query Match:	4.70%	Indels: 139
DB:	8	Gaps: 20

Qy	1057	GTGCACAAAGGGCAGAACCTGGGACATATGGGCCTGCACTATAGTGTAGGTCTGGTAGAG 1116
Db	3 09	RieserClyserArgantrpGlylleLeuvalLysIlepheGlyGlyLeuIleMet 328
Qy	1117	AATGTTATCATGGTCTGGTTT-----AAGTTC 1146
Db	3 29	HisPheIleMetGlyPheValPheLeuAsnValCysGlyPheProProAlaLeuGlnPhe 348
Qy	1147	TTGGAA---GNGAAAGTGTACTGAAATTAC-----TGTCAATCCTGATGTCCTTCTTCAG 1197
Db	3 49	PheGlyGluLeuTrpLeuValleAbnTyrlleThrIleGlyAspIleSerIleLeu 368
Qy	1198	CTCATTTATGCTTATCTGATTTC-----ATTGCTTCATGTCCTTCTTCAG 1248
Db	3 69	LeuValSerIleTyrllePheSerGlySerIleGlyPheIleIleItyrGlyLeuVal 388
Qy	1249	TACTGCAATCCATTGGCTCACTCTCACCCCTATAT-----GTAGTAGACTACCTCCAT 1302
Db	3 89	IleCysSerProIleAsnThrSerIleGlyLysSerGlyLeuAsnAsnPheLeuPhe 408
Qy	1303	TGTGTC 1308
Db	4 09	CysIle 410
RESULT 12		
Q9NUG5		PRELIMINARY; PRT; 223 AA.
ID	Q9NUG5	
AC	Q9NUG5;	
DT	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DB	DBJ 310013.4 (Novel protein similar to predicted <i>C. elegans</i> and <i>C. intestinalis</i> proteins) (Fragment).	
DE		
DN	DJ310013.4.	
OS	Homosapiens (Human).	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OC		
RN	[1] NC_0009606;	
RP	SEQUENCE FROM N.A.	
RA	Key M.;	
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.	
DR	AL031658; CAB88102.1; -.	
DR	Interru; IPR000504; RNA rec mot.	
DR	PROSTRE; PS000030; RRM RNP_1; UNKNOWN_1.	
DR	NON_TIER 1	
FT	NON_TIER 223	
FT	NON_TIER 223	
SQ	SEQUENCE 223 AA; 25490 MW; 78A0554C0329F70D CRC64;	
Alignment Scores:		
Pred. No.:	0.0108	Length: 223
Score:	119.00	Matches: 54
Percent Similarity:	42.80%	Conservative: 47
Best Local Similarity:	22.88%	Mismatches: 105
Query Match:	4.68%	Indels: 30
DB:	4	Gaps: 8
US-09-768-781-2 (1-1389) × Q9NUG5 (1-223)		
Qy	559	ATCCAGGCCCTCTGGCTCATGGCCAGCTATCAGCTCTATGTGAGCTGATC 618
Db	14	LeuGluIlePheLeuArgSerAlaPrgIleLeuValLeuIleSerIleLeuValHis 33
Qy	619	TCTGCAAGGGTCC---CTGGTAGGTTGCTATGGTATTTCCTGGPATCTGTC 675
Db	34	ArgGlyGlyIalaProAspIleLeuProAlaLeuSerThrSerAlaSerIleLeu 53
Qy	676	ACCTATGGGCCACCCCTGGCAATATCTGGCTATCCAGATCAAGTAGATGACTAACAG 735
Db	54	AlaTrp-----ThrIleAlaSerItyrGlnIlysValLeuArgAspSerArgAspAla 71
Qy	736	ATTCGCCCCCTGGGCCACTAGAAGTCCTCTGGCATACCCCTGGGACATTGGGATCACT 795







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Db 309 IleSerGlySerArgAntrpGlyIleeuvalysIlePheGlyGlyLeuIleMet 328
Qy 1117 ATGTTGATCATGCTCTGGTTT-----AACTTC 1146
Db 329 HisPheIleMetGlyPheValPheLeuAsnValCysGlyPheProProAlaLeuGlnPhe 348
Qy 1147 TTTGGA---GTCGAAGCTTACTGAAATTAC-----TGTCAATTCCCTGATTCCTGAG 1197
Db 349 PheGlyGluLeuIlePheValIleAsnIleIleAspIleIleSerLeuLeu 368
Qy 1198 CTCATTTATTCGCTTATCGATTTCC-----ATTCGCTTCATGCMCCCTTCTCCAG 1248
Db 369 LeuValIleSerIleIlePheSerGlySerIleIleGlyPheIleIleTyrglyLeuVal 388
Qy 1249 TACTGATCATTGGGTCACTCTCACCCATAAT-----GTAATGAGACTACCTCCAT 1302
Db 389 IleCysSerProIleAsnThrSerIleGluTyrSerGlyGlyLeuAspAsnPheLeuPhe 408
Qy 1303 TGTGTC 1308
Db 409 CysIle 410

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